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SEQUENCE LISTING

TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

- (i) APPLICANT: Kohei MIYAZONO; Takeshi IMAMURA; Peter DEN DIJKE
- (ii) TITLE OF INVENTION: ISOLATED ALK-1 PROTEIN, NUCLEIC ACIDS ENCODING IT, AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 46
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Fulbright & Jaworski L.L.P.  
(B) STREET: 801 Pennsylvania Avenue, N.W.  
(C) CITY: Washington  
(D) STATE: District of Columbia  
(E) COUNTRY: USA  
(F) ZIP: 20004
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb  
(B) COMPUTER: IBM PS/2  
(C) OPERATING SYSTEM: PC-DOS  
(D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/039,177  
(B) FILING DATE: March 13, 1998  
(C) CLASSIFICATION: 435
- E3  
(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: PCT/GB93/02367  
(B) FILING DATE: November 17, 1993
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: GB 9224057.1  
(B) FILING DATE: November 17, 1992
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: GB 9304677.9  
(B) FILING DATE: March 8, 1993
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: GB 9304680.3  
(B) FILING DATE: March 8, 1993
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 9311047.6  
(B) FILING DATE: May 28, 1993
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 9313763.6  
(B) FILING DATE: July 2, 1993



- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 9136099.2  
(B) FILING DATE: August 3, 1993
- (viii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 321344.5  
(B) FILING DATE: October 15, 1993
- (ix) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Mary Anne Schofield  
(B) REGISTRATION NUMBER: 36,669  
(C) REFERENCE/DOCKET NUMBER: LUD 5539 CIP - JEL/MAS
- (x) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (202) 662-0200  
(B) TELEFAX: (202) 662-4643
- (2) INFORMATION FOR SEQ ID NO: 1:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1984 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens
- (vii) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 283..1791
- (viii) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGCCA GGCAGGAAGA CGCTGGAATA	60
AGAAACATTT TTGCTCCAGC CCCCATCCC GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC	120
GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT	180
CCAGCGCTGG CGGTGCAACT GC GGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA	240
AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC	294
Met Thr Leu Gly	

TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln	5	10	15	20	342
GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys	25	30	35		390
GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr	40	45	50		438
GTA GTG CTG GTG CGG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly	55	60	65		486
TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe	70	75	80		534
GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser	85	90	95	100	582
CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp	105	110	115		630
GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu	120	125	130		678
GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA CGG AGG CAG GAG Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg Arg Arg Gln Glu	135	140	145		726
AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu	150	155	160		774
AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser	165	170	175	180	822
GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG Asp Cys Thr Thr Gly Ser Gly Leu Pro Phe Leu Val Gln Arg	185	190	195		870
ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly Lys Gly Arg	200	205	210		918
TAT GGC GAA GTG TGG CGG GGC TTG TGG CAC GGT GAG AGT GTG GCC GTC Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu Ser Val Ala Val					966

215	220	225	
AAG ATC TTC TCC TCG AGG GAT GAA CAG TCC TGG TTC CGG GAG ACT GAG Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg Glu Thr Glu 230	235	240	1014
ATC TAT AAC ACA GTA TTG CTC AGA CAC GAC AAC ATC CTA GGC TTC ATC Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu Gly Phe Ile 245	250	255	1062
GCC TCA GAC ATG ACC TCC CGC AAC TCG AGC ACG CAG CTG TGG CTC ATC Ala Ser Asp Met Thr Ser Arg Asn Ser Thr Gln Leu Trp Leu Ile 265	270	275	1110
ACG CAC TAC CAC GAG CAC GGC TCC CTC TAC GAC TTT CTG CAG AGA CAG Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln 280	285	290	1158
ACG CTG GAG CCC CAT CTG GCT CTG AGG CTA GCT GTG TCC GCG GCA TGC Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala Ala Cys 295	300	305	1206
GGC CTG GCG CAC CTG CAC GTG GAG ATC TTC GGT ACA CAG GGC AAA CCA Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro 310	315	320	1254
GCC ATT GCC CAC CGC GAC TTC AAG AGC CGC AAT GTG CTG GTC AAG AGC Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser 325	330	335	1302
AAC CTG CAG TGT TGC ATC GCC GAC CTG GGC CTG GCT GTG ATG CAC TCA Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser 345	350	355	1350
CAG GGC AGC GAT TAC CTG GAC ATC GGC AAC AAC CCG AGA GTG GGC ACC Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr 360	365	370	1398
AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp 375	380	385	1446
TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val 390	395	400	1494
CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp 405	410	415	1542
TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu 425	430	435	1590

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 104..1630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro	1638
440 445 450	
AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met	1686
455 460 465	
CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg	1734
470 475 480	
ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys	1782
485 490 495 500	
GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAAGGGGC Val Ile Gln	1831
TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGTA GAGGTAGTGT GAGTGTGGTG	1891
TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCCACCC AGCCAAAAAT	1951
ACAGCTGGGC TGAAACCTGA AAAAAAAAAAAA AAA	1984

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 503 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala	
1 5 10 15	
Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val	
20 25 30	
Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly	
35 40 45	
Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln	
50 55 60	
Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg	
65 70 75 80	
Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn	
85 90 95	
His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln	
100 105 110	
Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala	
115 120 125	
Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg	
130 135 140	

Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser  
 145 150 155 160  
 Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp  
 165 170 175  
 Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe  
 180 185 190  
 Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val  
 195 200 205  
 Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu  
 210 215 220  
 Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe  
 225 230 235 240  
 Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile  
 245 250 255  
 Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln  
 260 265 270  
 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe  
 275 280 285  
 Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val  
 290 295 300  
 Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr  
 305 310 315 320  
 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val  
 325 330 335  
 Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala  
 340 345 350  
 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro  
 355 360 365  
 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln  
 370 375 380  
 Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala  
 385 390 395 400  
 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly  
 405 410 415  
 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp  
 420 425 430  
 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr  
 435 440 445  
 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu  
 450 455 460  
 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu  
 465 470 475 480  
 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro  
 485 490 495  
 Glu Lys Pro Lys Val Ile Gln  
 500

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

TTC GCA GTA TGT CTT TTA GCC TGC CTG GGA GTT GCT CTC CGA AAA Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val Ala Leu Arg Lys 135 140 145	547
TTT AAA AGG CGC AAC CAA GAA CGC CTC AAT CCC CGA GAC GTG GAG TAT Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp Val Glu Tyr 150 155 160	595
GGC ACT ATC GAA GGG CTC ATC ACC ACC AAT GTT GGA GAC AGC ACT TTA Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp Ser Thr Leu 165 170 175 180	643
GCA GAT TTA TTG GAT CAT TCG TGT ACA TCA GGA AGT GGC TCT GGT CTT Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly Ser Gly Leu 185 190 195	691
CCT TTT CTG GTA CAA AGA ACA GTG GCT CGC CAG ATT ACA CTG TTG GAG Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr Leu Leu Glu 200 205 210	739
TGT GTC GGG AAA GGC AGG TAT GGT GAG GTG TGG AGG GGC AGC TGG CAA Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp Gln 215 220 225	787
GGG GAA AAT GTT GCC GTG AAG ATC TTC TCC TCC CGT GAT GAG AAG TCA Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Lys Ser 230 235 240	835
TGG TTC AGG GAA ACG GAA TTG TAC AAC ACT GTG ATG CTG AGG CAT GAA Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met Leu Arg His Glu 245 250 255 260	883
AAT ATC TTA GGT TTC ATT GCT TCA GAC ATG ACA TCA AGA CAC TCC AGT Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg His Ser Ser 265 270 275	931
ACC CAG CTG TGG TTA ATT ACA CAT TAT CAT GAA ATG GGA TCG TTG TAC Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met Gly Ser Leu Tyr 280 285 290	979
GAC TAT CTT CAG CTT ACT ACT CTG GAT ACA GTT AGC TGC CTT CGA ATA Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser Cys Leu Arg Ile 295 300 305	1027
GTG CTG TCC ATA GCT AGT GGT CTT GCA CAT TTG CAC ATA GAG ATA TTT Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His Ile Glu Ile Phe 310 315 320	1075
GGG ACC CAA GGG AAA CCA GCC ATT GCC CAT CGA GAT TTA AAG AGC AAA Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys 325 330 335 340	1123
AAT ATT CTG GTT AAG AAG AAT GGA CAG TGT TGC ATA GCA GAT TTG GGC Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile Ala Asp Leu Gly	1171

345	350	355	
CTG GCA GTC ATG CAT TCC CAG AGC ACC AAT CAG CTT GAT GTG GGG AAC Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu Asp Val Gly Asn 360	365	370	1219
AAT CCC CGT GTG GGC ACC AAG CGC TAC ATG GCC CCC GAA GTT CTA GAT Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp 375	380	385	1267
GAA ACC ATC CAG GTG GAT TGT TTC GAT TCT TAT AAA AGG GTC GAT ATT Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys Arg Val Asp Ile 390	395	400	1315
TGG GCC TTT GGA CTT GTT TTG TGG GAA GTG GCC AGG CGG ATG GTG AGC Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg Arg Met Val Ser 405	410	415	1363
AAT GGT ATA GTG GAG GAT TAC AAG CCA CCG TTC TAC GAT GTG GTT CCC Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr Asp Val Val Pro 425	430	435	1411
AAT GAC CCA AGT TTT GAA GAT ATG AGG AAG GTA GTC TGT GTG GAT CAA Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val Cys Val Asp Gln 440	445	450	1459
CAA AGG CCA AAC ATA CCC AAC AGA TGG TTC TCA GAC CCG ACA TTA ACC Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp Pro Thr Leu Thr 455	460	465	1507
TCT CTG GCC AAG CTA ATG AAA GAA TGC TGG TAT CAA AAT CCA TCC GCA Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln Asn Pro Ser Ala 470	475	480	1555
AGA CTC ACA GCA CTG CGT ATC AAA AAG ACT TTG ACC AAA ATT GAT AAT Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys Ile Asp Asn 485	490	495	1603
TCC CTC GAC AAA TTG AAA ACT GAC TGT TGACATTTTC ATAGTGTCAA Ser Leu Asp Lys Leu Lys Thr Asp Cys 505			1650
GAAGGAAGAT TTGACGTTGT TGTCATTGTC CAGCTGGAC CTAATGCTGG CCTGACTGGT 1710			
TGTCAGAATG GAATCCATCT GTCTCCCTCC CCAAATGGCT GCTTGACAA GGCAGACGTC 1770			
GTACCCAGCC ATGTGTTGGG GAGACATCAA AACCAACCCTA ACCTCGCTCG ATGACTGTGA 1830			
ACTGGGCATT TCACGAACTG TTCACACTGC AGAGACTAAT GTTGGACAGA CACTGTTGCA 1890			
AAGGTAGGGA CTGGAGGAAC ACAGAGAAAT CCTAAAAGAG ATCTGGCAT TAAGTCAGTG 1950			
GCTTGCATA GCTTTCACAA GTCTCCTAGA CACTCCCCAC GGGAAACTCA AGGAGGTGGT 2010			

GAATTTTAA TCAGCAATAT TGCCTGTGCT TCTCTTCTT ATTGCACTAG GAATTCTTG	2070
CATTCCTTAC TTGCACTGTT ACTCTTAATT TTAAAGACCC AACTTGCCAA AATGTTGGCT	2130
GCGTACTCCA CTGGTCTGTC TTTGGATAAT AGGAATTCAA TTTGGCAAAA CAAAATGTAA	2190
TGTCAGACTT TGCTGCATTT TACACATGTG CTGATGTTA CAATGATGCC GAACATTAGG	2250
AATTGTTTAT ACACAACATT GCAAATTATT TATTACTTGT GCACCTAGTA GTTTTACAA	2310
AACTGCTTTG TGCATATGTT AAAGCTTATT TTTATGTGGT CTTATGATT TATTACAGAA	2370
ATGTTTTAA CACTATACTC TAAAATGGAC ATTTCTTTT ATTATCAGTT AAAATCACAT	2430
TTTAAGTGCT TCACATTTGT ATGTGTGTAG ACTGTAACCTT TTTTCAGTT CATATGCAGA	2490
ACGTATTTAG CCATTACCCA CGTGACACCA CCGAATATAT TATCGATTAA GAAGCAAAGA	2550
TTTCAGTAGA ATTTAGTCC TGAACGCTAC GGGGAAAATG CATTTCCTTC AGAATTATCC	2610
ATTACGTGCA TTTAAACTCT GCCAGAAAAA AATAACTATT TTGTTTTAAT CTACTTTTG	2670
TATTTAGTAG TTATTTGTAT AAATTAAATA AACTGTTTTC AAGTCAAAAA AAAA	2724

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 509 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu			
1	5	10	15
Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu			
20	25	30	
Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys			
35	40	45	
Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His			
50	55	60	
Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr			
65	70	75	80
Cys Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly			
85	90	95	
Asp Trp Cys Asn Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys			
100	105	110	
Ser Phe Pro Gly Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile			
115	120	125	

Leu Ser Val Val Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val  
 130 135 140  
 Ala Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg  
 145 150 155 160  
 Asp Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly  
 165 170 175  
 Asp Ser Thr Leu Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser  
 180 185 190  
 Gly Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile  
 195 200 205  
 Thr Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg  
 210 215 220  
 Gly Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg  
 225 230 235 240  
 Asp Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met  
 245 250 255  
 Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser  
 260 265 270  
 Arg His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met  
 275 280 285  
 Gly Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser  
 290 295 300  
 Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His  
 305 310 315 320  
 Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp  
 325 330 335  
 Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile  
 340 345 350  
 Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu  
 355 360 365  
 Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro  
 370 375 380  
 Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys  
 385 390 395 400  
 Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg  
 405 410 415  
 Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr  
 420 425 430  
 Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val  
 435 440 445  
 Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp  
 450 455 460  
 Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln  
 465 470 475 480  
 Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr  
 485 490 495  
 Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys  
 500 505

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2932 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 310..1905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCTCCGCGCC	GAGGGCTGGA	GGATGCGTTC	CCTGGGTCC	GGACTTATGA	AAATATGCAT	60
CAGTTTAATA	CTGTCTTGGGA	ATTCATGAGA	TGGAAGCATA	GGTCAAAGCT	GTTTGGAGAA	120
AATCAGAAAGT	ACAGTTTTAT	CTAGCCACAT	CTTGGAGGAG	TCGTAAGAAA	GCAGTGAGGAG	180
TTGAAGTCAT	TGTCAAGTGC	TTGCGATCTT	TTACAAGAAA	ATCTCACTGA	ATGATAGTCA	240
TTTAAATTGG	TGAAGTAGCA	AGACCAATTAA	TTAAAGGTGA	CAGTACACAG	GAAACATTAC	300
AATTGAACA	ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC					348
Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala						
1	5		10			
TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG						396
Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met						
15	20		25			
CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA						444
Leu His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Ser Glu						
30	35		40		45	
AAT GGA GTA ACC TTA GCA CCA GAG GAT ACC TTG CCT TTT TTA AAG TGC						492
Asn Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys						
50	55		60			
TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC ACA TGC ATA						540
Tyr Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile						
65	70		75			
ACT AAT GGA CAT TGC TTT GCC ATC ATA GAA GAA GAT GAC CAG GGA GAA						588
Thr Asn Gly His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu						
80	85		90			

ACC ACA TTA GCT TCA GGG TGT ATG AAA TAT GAA GGA TCT GAT TTT CAG		636
Thr Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln		
95 100 105		
TGC AAA GAT TCT CCA AAA GCC CAG CTA CGC CGG ACA ATA GAA TGT TGT		684
Cys Lys Asp Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys		
110 115 120 125		
CGG ACC AAT TTA TGT AAC CAG TAT TTG CAA CCC ACA CTG CCC CCT GTT		732
Arg Thr Asn Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val		
130 135 140		
GTC ATA GGT CCG TTT TTT GAT GGC AGC ATT CGA TGG CTG GTT TTG CTC		780
Val Ile Gly Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu		
145 150 155		
ATT TCT ATG GCT GTC TGC ATA ATT GCT ATG ATC ATC TTC TCC AGC TGC		828
Ile Ser Met Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys		
160 165 170		
TTT TGT TAC AAA CAT TAT TGC AAG AGC ATC TCA AGC AGA CGT CGT TAC		876
Phe Cys Tyr Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr		
175 180 185		
AAT CGT GAT TTG GAA CAG GAT GAA GCA TTT ATT CCA GTT GGA GAA TCA		924
Asn Arg Asp Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser		
190 195 200 205		
CTA AAA GAC CTT ATT GAC CAG TCA CAA AGT TCT GGT AGT GGG TCT GGA		972
Leu Lys Asp Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly		
210 215 220		
CTA CCT TTA TTG GTT CAG CGA ACT ATT GCC AAA CAG ATT CAG ATG GTC		1020
Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val		
225 230 235		
CGG CAA GTT GGT AAA GGC CGA TAT GGA GAA GTA TGG ATG GGC AAA TGG		1068
Arg Gln Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp		
240 245 250		
CGT GGC GAA AAA GTG GCG GTG AAA GTA TTC TTT ACC ACT GAA GAA GCC		1116
Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala		
255 260 265		
AGC TGG TTT CGA GAA ACA GAA ATC TAC CAA ACT GTG CTA ATG CGC CAT		1164
Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His		
270 275 280 285		
GAA AAC ATA CTT GGT TTC ATA GCG GCA GAC ATT AAA GGT ACA GGT TCC		1212
Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser		
290 295 300		
TGG ACT CAG CTC TAT TTG ATT ACT GAT TAC CAT GAA AAT GGA TCT CTC		1260
Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu		

305

310

315

TAT GAC TTC CTG AAA TGT GCT ACA CTG GAC ACC AGA GCC CTG CTT AAA Tyr Asp Phe Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys 320	325	330	1308
TTG GCT TAT TCA GCT GCC TGT GGT CTG TGC CAC CTG CAC ACA GAA ATT Leu Ala Tyr Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile 335	340	345	1356
TAT GGC ACC CAA GGA AAG CCC GCA ATT GCT CAT CGA GAC CTA AAG AGC Tyr Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser 350	355	360	1404
AAA AAC ATC CTC ATC AAG AAA AAT GGG AGT TGC TGC ATT GCT GAC CTG Lys Asn Ile Leu Ile Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu 370	375	380	1452
GGC CTT GCT GTT AAA TTC AAC AGT GAC ACA AAT GAA GTT GAT GTG CCC Gly Leu Ala Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro 385	390	395	1500
TTG AAT ACC AGG GTG GGC ACC AAA CGC TAC ATG GCT CCC GAA GTG CTG Leu Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu 400	405	410	1548
GAC GAA AGC CTG AAC AAA AAC CAC TTC CAG CCC TAC ATC ATG GCT GAC Asp Glu Ser Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp 415	420	425	1596
ATC TAC AGC TTC GGC CTA ATC ATT TGG GAG ATG GCT CGT CGT TGT ATC Ile Tyr Ser Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile 430	435	440	1644
ACA GGA GGG ATC GTG GAA GAA TAC CAA TTG CCA TAT TAC AAC ATG GTA Thr Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val 450	455	460	1692
CCG AGT GAT CCG TCA TAC GAA GAT ATG CGT GAG GTT GTG TGT GTC AAA Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys 465	470	475	1740
CGT TTG CGG CCA ATT GTG TCT AAT CGG TGG AAC AGT GAT GAA TGT CTA Arg Leu Arg Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu 480	485	490	1788
CGA GCA GTT TTG AAG CTA ATG TCA GAA TGC TGG GCC CAC AAT CCA GCC Arg Ala Val Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala 495	500	505	1836
TCC AGA CTC ACA GCA TTG AGA ATT AAG AAG ACG CTT GCC AAG ATG GTT Ser Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val 510	515	520	1884
		525	

GAA TCC CAA GAT GTA AAA ATC TGATGGTTAA ACCATCGGAG GAGAAACTCT	1935
Glu Ser Gln Asp Val Lys Ile	
530	
AGACTGCAAG AACTGTTTT ACCCATGGCA TGGGTGGAAT TAGAGTGGAA TAAGGATGTT	1995
AACTTGGTTC TCAGACTCTT TCTTCACTAC GTGTCACAG GCTGCTAATA TTAAACCTTT	2055
CAGTACTCTT ATTAGGATAC AAGCTGGAA CTTCTAAACA CTTCATTCTT TATATATGGA	2115
CAGCTTTATT TTAAATGTGG TTTTGATGC CTTTTTTAA GTGGGTTTT ATGAAC TGCA	2175
TCAAGACTTC AATCCTGATT AGTGTCTCCA GTCAAGCTCT GGGTACTGAA TTGCCTGTT	2235
ATAAAACGGT GCTTCTGTG AAAGCCTAA GAAGATAAAT GAGCGCAGCA GAGATGGAGA	2295
AATAGACTTT GCCTTTACC TGAGACATTC AGTCGTTG TATTCTACCT TTGTAAAACA	2355
GCCTATAGAT GATGATGTGT TTGGGATACT GCTTATTTA TGATAGTTG TCCTGTGTCC	2415
TTAGTGATGT GTGTGTGTCT CCATGCACAT GCACGCCGGG ATTCCTCTGC TGCCATTGTA	2475
ATTAGAAGAA AATAATTAT ATGCATGCAC AGGAAGATAT TGGTGGCCGG TGGTTTGTG	2535
CTTTAAAAAT GCAATATCTG ACCAAGATTG GCCAATCTCA TACAAGCCAT TTACTTGCA	2595
AGTGAGATAG CTTCCCCACC AGCTTATT TTTAACATGA AAGCTGATGC CAAGGCCAAA	2655
AGAAGTTAA AGCATCTGTA AATTTGGACT GTTTCCCTTC AACCAACCATT TTTTTGTGG	2715
TTATTATTT TGTCACGGAA AGCATCCTCT CCAAAGTTGG AGCTTCTATT GCCATGAACC	2775
ATGCTTACAA AGAAAGCACT TCTTATTGAA GTGAATTCT GCATTTGATA GCAATGTAAG	2835
TGCCTATAAC CATGTTCTAT ATTCTTTATT CTCAGTAACT TTTAAAAGGG AAGTTATTAA	2895
TATTTGTGT ATAATGTGCT TTATTTGCAA ATCACCC	2932

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 532 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala Tyr Leu Phe			
1	5	10	15
Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly			
20	25	30	
Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu Asn Gly Val			

35                    40                    45

Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser  
50                    55                    60

Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly  
65                    70                    75                    80

His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu  
85                    90                    95

Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp  
100                    105                    110

Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn  
115                    120                    125

Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly  
130                    135                    140

Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu Ile Ser Met  
145                    150                    155                    160

Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr  
165                    170                    175

Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr Asn Arg Asp  
180                    185                    190

Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp  
195                    200                    205

Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Leu Pro Leu  
210                    215                    220

Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val  
225                    230                    235                    240

Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu  
245                    250                    255

Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe  
260                    265                    270

Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile  
275                    280                    285

Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln  
290                    295                    300

Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe  
305                    310                    315                    320

Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr  
325                    330                    335

Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr  
340                    345                    350

Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile  
355                    360                    365

Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala  
370                    375                    380

Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro Leu Asn Thr  
385                    390                    395                    400

Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser  
405                    410                    415

Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser  
420                    425                    430

Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly  
435                    440                    445

Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp  
450                    455                    460

Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg

465	470	475	480
Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val			
485	490	495	
Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu			
500	505	510	
Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln			
515	520	525	
Asp Val Lys Ile			
530			

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 2333 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..1515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT GTT GTC CTC	48		
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu			
1	5	10	15
CTG CTC GCC GGC AGC GGG TCC GGG CCC CGG GGG GTC CAG GCT CTG	96		
Leu Leu Ala Gly Ser Gly Ser Gly Pro Arg Gly Val Gln Ala Leu			
20	25	30	
CTG TGT GCG TGC ACC AGC TGC CTC CAG GCC AAC TAC ACG TGT GAG ACA	144		
Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr			
35	40	45	
GAT GGG GCC TGC ATG GTT TCC TTT TTC AAT CTG GAT GGG ATG GAG CAC	192		
Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His			
50	55	60	
CAT GTG CGC ACC TGC ATC CCC AAA GTG GAG CTG GTC CCT GCC GGG AAG	240		
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys			
65	70	75	80

CCC TTC TAC TGC CTG AGC TCG GAG GAC CTG CGC AAC ACC CAC TGC TGC Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys	288
85 90 95	
TAC ACT GAC TAC TGC AAC AGG ATC GAC TTG AGG GTG CCC AGT GGT CAC Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His	336
100 105 110	
CTC AAG GAG CCT GAG CAC CCG TCC ATG TGG GGC CCG GTG GAG CTG GTA Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val	384
115 120 125	
GGC ATC ATC GCC GGC CCG GTG TTC CTC CTG TTC CTC ATC ATC ATT Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile	432
130 135 140	
GTT TTC CTT GTC ATT AAC TAT CAT CAG CGT GTC TAT CAC AAC CGC CAG Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln	480
145 150 155 160	
AGA CTG GAC ATG GAA GAT CCC TCA TGT GAG ATG TGT CTC TCC AAA GAC Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp	528
165 170 175	
AAG ACG CTC CAG GAT CTT GTC TAC GAT CTC TCC ACC TCA GGG TCT GGC Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly	576
180 185 190	
TCA GGG TTA CCC CTC TTT GTC CAG CGC ACA GTG GCC CGA ACC ATC GTT Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val	624
195 200 205	
TTA CAA GAG ATT ATT GGC AAG GGT CGG TTT GGG GAA GTA TGG CGG GGC Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly	672
210 215 220	
CGC TGG AGG GGT GAT GTG GCT GTG AAA ATA TTC TCT TCT CGT GAA Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu	720
225 230 235 240	
GAA CGG TCT TGG TTC AGG GAA GCA GAG ATA TAC CAG ACG GTC ATG CTG Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu	768
245 250 255	
245 250 255	
CGC CAT GAA AAC ATC CTT GGA TTT ATT GCT GCT GAC AAT AAA GAT AAT Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn	816
260 265 270	
GGA ACC TGG ACA CAG CTG TGG CTT GTT TCT GAC TAT CAT GAG CAC GGG Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly	864
275 280 285	
TCC CTG TTT GAT TAT CTG AAC CGG TAC ACA GTG ACA ATT GAG GGG ATG Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met	912
290 295 300	

ATT AAG CTG GCC TTG TCT GCT GCT AGT GGG CTG GCA CAC CTG CAC ATG Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met	305	310	315	320	960
GAG ATC GTG GGC ACC CAA GGG AAG CCT GGA ATT GCT CAT CGA GAC TTA Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu	325	330	335		1008
AAG TCA AAG AAC ATT CTG GTG AAG AAA AAT GGC ATG TGT GCC ATA GCA Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala	340	345	350		1056
GAC CTG GGC CTG GCT GTC CGT CAT GAT GCA GTC ACT GAC ACC ATT GAC Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp	355	360	365		1104
ATT GCC CCG AAT CAG AGG GTG GGG ACC AAA CGA TAC ATG GCC CCT GAA Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu	370	375	380		1152
GTA CTT GAT GAA ACC ATT AAT ATG AAA CAC TTT GAC TCC TTT AAA TGT Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys	385	390	395	400	1200
GCT GAT ATT TAT GCC CTC GGG CTT GTA TAT TGG GAG ATT GCT CGA AGA Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg	405	410	415		1248
TGC AAT TCT GGA GGA GTC CAT GAA GAA TAT CAG CTG CCA TAT TAC GAC Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp	420	425	430		1296
TTA GTG CCC TCT GAC CCT TCC ATT GAG GAA ATG CGA AAG GTT GTA TGT Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys	435	440	445		1344
GAT CAG AAG CTG CGT CCC AAC ATC CCC AAC TGG TGG CAG AGT TAT GAG Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu	450	455	460		1392
GCA CTG CGG GTG ATG GGG AAG ATG ATG CGA GAG TGT TGG TAT GCC AAC Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn	465	470	475	480	1440

GGC GCA GCC CGC CTG ACG GCC CTG CGC ATC AAG AAG ACC CTC TCC CAG	1488	
Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln		
485	490	495
CTC AGC GTG CAG GAA GAC GTG AAG ATC TAACTGCTCC CTCTCTCCAC	1535	
Leu Ser Val Gln Glu Asp Val Lys Ile		
500	505	
ACGGAGCTCC TGGCAGCGAG AACTACGCAC AGCTGCCGCG TTGAGCGTAC GATGGAGGCC	1595	
TACCTCTCGT TTCTGCCAG CCCTCTGTGG CCAGGAGCCC TGGCCCGCAA GAGGGACAGA	1655	
GCCCCGGAGA GACTCGCTCA CTCCCATGTT GGGTTGAGA CAGACACCTT TTCTATTTAC	1715	
CTCCTAATGG CATGGAGACT CTGAGAGCGA ATTGTGTGGA GAACTCAGTG CCACACCTCG	1775	
AACTGGTTGT AGTGGGAAGT CCCGCGAAAC CCGGTGCATC TGGCACGTGG CCAGGAGCCA	1835	
TGACAGGGGC GCTTGGGAGG GGCCGGAGGA ACCGAGGTGT TGCCAGTGCT AAGCTGCCCT	1895	
GAGGGTTTCC TTCGGGGACC AGCCCACAGC ACACCAAGGT GGCCCGGAAG AACCAGAAGT	1955	
GCAGCCCCCTC TCACAGGCAG CTCTGAGCCG CGCTTCCCC TCCTCCCTGG GATGGACGCT	2015	
GCCGGGAGAC TGCCAGTGGA GACGGAATCT GCCGCTTGT CTGTCCAGCC GTGTGTGCAT	2075	
GTGCCGAGGT GCGTCCCCCG TTGTGCCTGG TTCGTGCCAT GCCCTTACAC GTGCGTGTGA	2135	
GTGTGTGTGT GTGTCTGTAG GTGCGCACTT ACCTGCTTGA GCTTTCTGTG CATGTGCAGG	2195	
TCGGGGGTGT GGTCGTCATG CTGTCCGTGC TTGCTGGTGC CTCTTTCAAG TAGTGAGCAG	2255	
CATCTAGTTT CCCTGGTGCC CTTCCCTGGA GGTCTCTCCC TCCCCAGAG CCCCTCATGC	2315	
CACAGTGGTA CTCTGTGT	2333	

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 505 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu			
1	5	10	15
Leu Leu Ala Gly Ser Gly Ser Gly Pro Arg Gly Val Gln Ala Leu			
20	25	30	
Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr			
35	40	45	

Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His  
50 55 60  
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys  
65 70 75 80  
Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys  
85 90 95  
Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His  
100 105 110  
Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val  
115 120 125  
Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile  
130 135 140  
Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln  
145 150 155 160  
Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp  
165 170 175  
Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly  
180 185 190  
Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val  
195 200 205  
Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly  
210 215 220  
Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu  
225 230 235 240  
Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu  
245 250 255  
Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn  
260 265 270  
Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly  
275 280 285  
Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met  
290 295 300  
Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met  
305 310 315 320  
Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu  
325 330 335  
Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala  
340 345 350  
Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp  
355 360 365  
Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu  
370 375 380  
Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys  
385 390 395 400  
Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg  
405 410 415  
Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp  
420 425 430  
Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys  
435 440 445  
Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu  
450 455 460  
Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn  
465 470 475 480

Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln  
                   485                  490                  495  
  Leu Ser Val Gln Glu Asp Val Lys Ile  
                   500                  505

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2308 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: unknown
    - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 77..1585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGCGAGGCAGA GGTTTGCTGG GGTGAGGCAG CGGCGCGGCC GGGCCGGGCC GGGCCACAGG 60

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CGGTGGCGGC GGGACC ATG GAG GCG GCG GTC GCT GCT CCG CGT CCC CGG      109
          Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg
          1           5           10

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CTC CCG GGG GCG ACG GCG TTA CAG TGT TTC TGC CAC CTC TGT ACA AAA  
 Leu Pro Gly Ala Thr Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys  
 30 35 40

GAC AAT TTT ACT TGT GTG ACA GAT GGG CTC TGC TTT GTC TCT GTC ACA  
Asp Asn Phe Thr Cys Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr  
45 50 55

GAG ACC ACA GAC AAA GTT ATA CAC AAC AGC ATG TGT ATA GCT GAA ATT  
 Glu Thr Thr Asp Lys Val Ile His Asn Ser Met Cys Ile Ala Glu Ile  
 60 65 70 75

GAC TTA ATT CCT CGA GAT AGG CCG TTT GTA TGT GCA CCC TCT TCA AAA 349  
Asp Leu Ile Pro Arg Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys

80	85	90	
ACT GGG TCT GTG ACT ACA ACA TAT TGC TGC AAT CAG GAC CAT TGC AAT Thr Gly Ser Val Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn 95	100	105	397
AAA ATA GAA CTT CCA ACT ACT GTA AAG TCA TCA CCT GGC CTT GGT CCT Lys Ile Glu Leu Pro Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro 110	115	120	445
GTG GAA CTG GCA GCT GTC ATT GCT GGA CCA GTG TGC TTC GTC TGC ATC Val Glu Leu Ala Ala Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile 125	130	135	493
TCA CTC ATG TTG ATG GTC TAT ATC TGC CAC AAC CGC ACT GTC ATT CAC Ser Leu Met Leu Met Val Tyr Ile Cys His Asn Arg Thr Val Ile His 140	145	150	541
CAT CGA GTG CCA AAT GAA GAG GAC CCT TCA TTA GAT CGC CCT TTT ATT His Arg Val Pro Asn Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile 160	165	170	589
TCA GAG GGT ACT ACG TTG AAA GAC TTA ATT TAT GAT ATG ACA ACG TCA Ser Glu Gly Thr Thr Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser 175	180	185	637
GGT TCT GGC TCA GGT TTA CCA TTG CTT GTT CAG AGA ACA ATT GCG AGA Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg 190	195	200	685
ACT ATT GTG TTA CAA GAA AGC ATT GGC AAA GGT CGA TTT GGA GAA GTT Thr Ile Val Leu Gln Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val 205	210	215	733
TGG AGA GGA AAG TGG CGG GGA GAA GAA GTT GCT GTT AAG ATA TTC TCC Trp Arg Gly Lys Trp Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser 220	225	230	781
TCT AGA GAA GAA CGT TCG TGG TTC CGT GAG GCA GAG ATT TAT CAA ACT Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr 240	245	250	829
GTA ATG TTA CGT CAT GAA AAC ATC CTG GGA TTT ATA GCA GCA GAC AAT Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn 255	260	265	877
AAA GAC AAT GGT ACT TGG ACT CAG CTC TGG TTG GTG TCA GAT TAT CAT Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His 270	275	280	925
GAG CAT GGA TCC CTT TTT GAT TAC TTA AAC AGA TAC ACA GTT ACT GTG Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val 285	290	295	973

GAA GGA ATG ATA AAA CTT GCT CTG TCC ACG GCG AGC GGT CTT GCC CAT Glu Gly Met Ile Lys Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His 300                   305                   310                   315	1021
CTT CAC ATG GAG ATT GTT GGT ACC CAA GGA AAG CCA GCC ATT GCT CAT Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His 320                   325                   330	1069
AGA GAT TTG AAA TCA AAG AAT ATC TTG GTA AAG AAG AAT GGA ACT TGC Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys 335                   340                   345	1117
TGT ATT GCA GAC TTA GGA CTG GCA GTA AGA CAT GAT TCA GCC ACA GAT Cys Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp 350                   355                   360	1165
ACC ATT GAT ATT GCT CCA AAC CAC AGA GTG GGA ACA AAA AGG TAC ATG Thr Ile Asp Ile Ala Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met 365                   370                   375	1213
GCC CCT GAA GTT CTC GAT GAT TCC ATA AAT ATG AAA CAT TTT GAA TCC Ala Pro Glu Val Leu Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser 380                   385                   390                   395	1261
TTC AAA CGT GCT GAC ATC TAT GCA ATG GGC TTA GTA TTC TGG GAA ATT Phe Lys Arg Ala Asp Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile 400                   405                   410	1309
GCT CGA CGA TGT TCC ATT GGT GGA ATT CAT GAA GAT TAC CAA CTG CCT Ala Arg Arg Cys Ser Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro 415                   420                   425	1357
TAT TAT GAT CTT GTA CCT TCT GAC CCA TCA GTT GAA GAA ATG AGA AAA Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys 430                   435                   440	1405
GTT GTT TGT GAA CAG AAG TTA AGG CCA AAT ATC CCA AAC AGA TGG CAG Val Val Cys Glu Gln Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln 445                   450                   455	1453
AGC TGT GAA GCC TTG AGA GTA ATG GCT AAA ATT ATG AGA GAA TGT TGG Ser Cys Glu Ala Leu Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp 460                   465                   470                   475	1501
TAT GCC AAT GGA GCA GCT AGG CTT ACA GCA TTG CGG ATT AAG AAA ACA Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr 480                   485                   490	1549
TTA TCG CAA CTC AGT CAA CAG GAA GGC ATC AAA ATG TAATTCTACA Leu Ser Gln Leu Ser Gln Gln Glu Gly Ile Lys Met 495                   500	1595
GCTTTGCCTG AACTCTCCTT TTTTCTTCAG ATCTGCTCCT GGGTTTTAAT TTGGGAGGTC	1655

AGTTGTTCTA CCTCACTGAG AGGAAACAGA AGGATATTGC TTCCTTTGC AGCAGTGTAA	1715
TAAAGTCAAT TAAAAACTTC CCAGGATTC TTTGGACCCA GGAAACAGCC ATGTGGGTCC	1775
TTTCTGTGCA CTATGAACGC TTCTTCCCCA GGACAGAAAA TGTGTAGTCT ACCTTTATTT	1835
TTTATTAACA AAACTTGTTT TTTAAAAGA TGATTGCTGG TCTTAACCTT AGGTAACTCT	1895
GCTGTGCTGG AGATCATCTT TAAGGGCAAA GGAGTTGGAT TGCTGAATTA CAATGAAACA	1955
TGTCTTATTA CTAAAGAAAG TGATTTACTC CTGGTTAGTA CATTCTCAGA GGATTCTGAA	2015
CCACTAGAGT TTCCTTGATT CAGACTTTGA ATGTACTGTT CTATAGTTT TCAGGATCTT	2075
AAAACATAACA CTTATAAAC TCTTATCTTG AGTCTAAAAA TGACCTCATA TAGTAGTGAG	2135
GAACATAATT CATGCAATTG TATTTGTAT ACTATTATTG TTCTTCACT TATTCAGAAC	2195
ATTACATGCC TTCAAAATGG GATTGTACTA TACCAAGTAAG TGCCACTTCT GTGTCTTCT	2255
AATGGAAATG AGTAGAATTG CTGAAAGTCT CTATGTTAAA ACCTATAGTG TTT	2308

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 503 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

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Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg Leu Leu Leu Leu Val
   1           5           10          15
Leu Ala Ala Ala Ala Ala Ala Ala Leu Leu Pro Gly Ala Thr
   20          25          30
Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr Cys
   35          40          45
Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr Glu Thr Thr Asp Lys
   50          55          60
Val Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg
   65          70          75          80
Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ser Val Thr
   85          .         90          95
Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro
  100          105         110
Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro Val Glu Leu Ala Ala
  115          120         125
Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile Ser Leu Met Leu Met
  130          135         140
Val Tyr Ile Cys His Asn Arg Thr Val Ile His His Arg Val Pro Asn
  145          150         155          160
Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile Ser Glu Gly Thr Thr

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165	170	175
Leu Lys Asp Leu Ile Tyr Asp Met	Thr Thr Ser Gly Ser Gly	
180	185	190
Leu Pro Leu Leu Val Gln Arg	Thr Ile Ala Arg Thr	Ile Val Leu Gln
195	200	205
Glu Ser Ile Gly Lys Gly Arg	Phe Gly Glu Val Trp Arg	Gly Lys Trp
210	215	220
Arg Gly Glu Glu Val Ala Val	Lys Ile Phe Ser Ser Arg	Glu Glu Arg
225	230	235
Ser Trp Phe Arg Glu Ala Glu	Ile Tyr Gln Thr Val Met	Leu Arg His
245	250	255
Glu Asn Ile Leu Gly Phe Ile Ala Ala	Asp Asn Lys Asp Asn Gly	Thr
260	265	270
Trp Thr Gln Leu Trp Leu Val	Ser Asp Tyr His Glu His	Gly Ser Leu
275	280	285
Phe Asp Tyr Leu Asn Arg	Tyr Thr Val Thr Val	Glu Gly Met Ile Lys
290	295	300
Leu Ala Leu Ser Thr Ala Ser	Gly Leu Ala His	Leu His Met Glu Ile
305	310	315
Val Gly Thr Gln Gly Lys Pro	Ala Ile Ala His Arg Asp	Leu Lys Ser
325	330	335
Lys Asn Ile Leu Val Lys Lys	Asn Gly Thr Cys Cys	Ile Ala Asp Leu
340	345	350
Gly Leu Ala Val Arg His	Asp Ser Ala Thr Asp Thr	Ile Asp Ile Ala
355	360	365
Pro Asn His Arg Val Gly	Thr Lys Arg Tyr Met	Ala Pro Glu Val Leu
370	375	380
Asp Asp Ser Ile Asn Met	Lys His Phe Glu Ser Phe	Lys Arg Ala Asp
385	390	395
Ile Tyr Ala Met Gly Leu Val	Phe Trp Glu Ile Ala Arg	Arg Cys Ser
405	410	415
Ile Gly Gly Ile His Glu Asp	Tyr Gln Leu Pro Tyr Tyr	Asp Leu Val
420	425	430
Pro Ser Asp Pro Ser Val	Glu Met Arg Lys Val Val	Cys Glu Gln
435	440	445
Lys Leu Arg Pro Asn Ile Pro	Asn Arg Trp Gln Ser Cys	Glu Ala Leu
450	455	460
Arg Val Met Ala Lys Ile Met	Arg Glu Cys Trp Tyr	Ala Asn Gly Ala
465	470	475
Ala Arg Leu Thr Ala Leu Arg	Ile Lys Lys Thr	Leu Ser Gln Leu Ser
485	490	495
Gln Gln Glu Gly Ile Lys Met		
500		

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1922 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 241..1746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GAGAGCACAG CCCTTCCCAG TCCCCGGAGC CGCCGCGCCA CGCGCGCATG ATCAAGACCT	60
TTTCCCCGGC CCCACAGGGC CTCTGGACGT GAGACCCCGG CCGCCTCCGC AAGGAGAGGC	120
GGGGGTCGAG TCGCCCTGTC CAAAGGCCTC AATCTAAACA ATCTTGATTC CTGTTGCCGG	180
CTGGCGGGAC CCTGAATGGC AGGAAATCTC ACCACATCTC TTCTCCTATC TCCAAGGACC	240
ATG ACC TTG GGG AGC TTC AGA AGG GGC CTT TTG ATG CTG TCG GTG GCC	288
Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala	
1 5 10 15	
TTG GGC CTA ACC CAG GGG AGA CTT GCG AAG CCT TCC AAG CTG GTG AAC	336
Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn	
20 25 30	
TGC ACT TGT GAG AGC CCA CAC TGC AAG AGA CCA TTC TGC CAG GGG TCA	384
Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser	
35 40 45	
TGG TGC ACA GTG GTG CTG GTT CGA GAG CAG GGC AGG CAC CCC CAG GTC	432
Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val	
50 55 60	
TAT CGG GGC TGT GGG AGC CTG AAC CAG GAG CTC TGC TTG GGA CGT CCC	480
Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro	
65 70 75 80	
ACG GAG TTT CTG AAC CAT CAC TGC TGC TAT AGA TCC TTC TGC AAC CAC	528
Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His	
85 90 95	
AAC GTG TCT CTG ATG CTG GAG GCC ACC CAA ACT CCT TCG GAG GAG CCA	576
Asn Val Ser Leu Met Leu Glu Ala Thr Gln Thr Pro Ser Glu Glu Pro	
100 105 110	
GAA GTT GAT GCC CAT CTG CCT CTG ATC CTG GGT CCT GTG CTG GCC TTG	624
Glu Val Asp Ala His Leu Pro Leu Ile Leu Gly Pro Val Leu Ala Leu	
115 120 125	

CCG GTC CTG GTG GCC CTG GGT GCT CTG GGC TTG TGG CGT GTC CGG CGG Pro Val Leu Val Ala Leu Gly Ala Leu Gly Leu Trp Arg Val Arg Arg	130                    135                    140	672
AGG CAG GAG AAG CAG CGG GAT TTG CAC AGT GAC CTG GGC GAG TCC AGT Arg Gln Glu Lys Gln Arg Asp Leu His Ser Asp Leu Gly Glu Ser Ser	145                    150                    155                    160	720
CTC ATC CTG AAG GCA TCT GAA CAG GCA GAC AGC ATG TTG GGG GAC TTC Leu Ile Leu Lys Ala Ser Glu Gln Ala Asp Ser Met Leu Gly Asp Phe	165                    . 170                    175	768
CTG GAC AGC GAC TGT ACC ACG GGC AGC GGC TCG GGG CTC CCC TTC TTG Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu	180                    185                    190	816
GTG CAG AGG ACG GTA GCT CGG CAG GTT GCG CTG GTA GAG TGT GTG GGA Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly	195                    200                    205	864
AAG GGC CGA TAT GGC GAG GTG TGG CGC GGT TCG TGG CAT GGC GAA AGC Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp His Gly Glu Ser	210                    215                    220	912
GTG GCG GTC AAG ATT TTC TCC TCA CGA GAT GAG CAG TCC TGG TTC CGG Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg	225                    230                    235                    240	960
GAG ACG GAG ATC TAC AAC ACA GTT CTG CTT AGA CAC GAC AAC ATC CTA Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu	245                    250                    255	1008
GGC TTC ATC GCC TCC GAC ATG ACT TCG CGG AAC TCG AGC ACG CAG CTG Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu	260                    265                    270	1056
TGG CTC ATC ACC CAC TAC CAT GAA CAC GGC TCC CTC TAT GAC TTT CTG Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu	275                    280                    285	1104
CAG AGG CAG ACG CTG GAG CCC CAG TTG GCC CTG AGG CTA GCT GTG TCC Gln Arg Gln Thr Leu Glu Pro Gln Leu Ala Leu Arg Leu Ala Val Ser	290                    295                    300	1152
CCG GCC TGC GGC CTG GCG CAC CTA CAT GTG GAG ATC TTT GGC ACT CAA Pro Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln	305                    310                    315                    320	1200
GGC AAA CCA GCC ATT GCC CAT CGT GAC CTC AAG AGT CGC AAT GTG CTG Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Arg Asn Val Leu	325                    330                    335	1248
GTC AAG AGT AAC TTG CAG TGT TGC ATT GCA GAC CTG GGA CTG GCT GTG Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val		1296

340	345	350	
ATG CAC TCA CAA AGC AAC GAG TAC CTG GAT ATC GGC AAC ACA CCC CGA Met His Ser Gln Ser Asn Glu Tyr Leu Asp Ile Gly Asn Thr Pro Arg			1344
355	360	365	
GTG GGT ACC AAA AGA TAC ATG GCA CCC GAG GTG CTG GAT GAG CAC ATC Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu His Ile			1392
370	375	380	
CGC ACA GAC TGC TTT GAG TCG TAC AAG TGG ACA GAC ATC TGG GCC TTT Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe			1440
385	390	395	400
GGC CTA GTG CTA TGG GAG ATC GCC CGG CGG ACC ATC ATC AAT GGC ATT Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile			1488
405	410	415	
GTC GAG GAT TAC AGG CCA CCT TTC TAT GAC ATG GTA CCC AAT GAC CCC Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro			1536
420	425	430	
AGT TTT GAG GAC ATG AAA AAG GTG GTG TGC GTT GAC CAG CAG ACA CCC Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro			1584
435	440	445	
ACC ATC CCT AAC CGG CTG GCT GCA GAT CCG GTC CTC TCC GGG CTG GCC Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala			1632
450	455	460	
CAG ATG ATG AGA GAG TGC TGG TAC CCC AAC CCC TCT GCT CGC CTC ACC Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr			1680
465	470	475	480
GCA CTG CGC ATA AAG AAG ACA TTG CAG AAG CTC AGT CAC AAT CCA GAG Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu			1728
485	490	495	
AAG CCC AAA GTG ATT CAC TAGCCCAGGG CCACCCAGGCT TCCTCTGCCT Lys Pro Lys Val Ile His			1776
500			
AAAGTGTGTG CTGGGAAGA AGACATAGCC TGTCTGGTA GAGGGAGTGA AGAGAGTGTG			1836
CACGCTGCC TGTGTGTGCC TGCTCAGCTT GCTCCCAGCC CATCCAGCCA AAAATACAGC			1896
TGAGCTGAAA TTCAAAAAAA AAAAAAA			1922

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 502 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala  
1 5 10 15  
Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn  
20 25 30  
Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser  
35 40 45  
Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val  
50 55 60  
Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro  
65 70 75 80  
Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His  
85 90 95  
Asn Val Ser Leu Met Leu Glu Ala Thr Gln Thr Pro Ser Glu Glu Pro  
100 105 110  
Glu Val Asp Ala His Leu Pro Leu Ile Leu Gly Pro Val Leu Ala Leu  
115 120 125  
Pro Val Leu Val Ala Leu Gly Ala Leu Gly Leu Trp Arg Val Arg Arg  
130 135 140  
Arg Gln Glu Lys Gln Arg Asp Leu His Ser Asp Leu Gly Glu Ser Ser  
145 150 155 160  
Leu Ile Leu Lys Ala Ser Glu Gln Ala Asp Ser Met Leu Gly Asp Phe  
165 170 175  
Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Leu Pro Phe Leu  
180 185 190  
Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly  
195 200 205  
Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp His Gly Glu Ser  
210 215 220  
Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg  
225 230 235 240  
Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu  
245 250 255  
Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu  
260 265 270  
Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu  
275 280 285  
Gln Arg Gln Thr Leu Glu Pro Gln Leu Ala Leu Arg Leu Ala Val Ser  
290 295 300  
Pro Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln  
305 310 315 320  
Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Arg Asn Val Leu  
325 330 335  
Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val  
340 345 350  
Met His Ser Gln Ser Asn Glu Tyr Leu Asp Ile Gly Asn Thr Pro Arg  
355 360 365  
Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu His Ile  
370 375 380  
Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe  
385 390 395 400

Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile  
                   405                  410                  415  
 Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro  
                   420                  425                  430  
 Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro  
                   435                  440                  445  
 Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala  
                   450                  455                  460  
 Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr  
                   465                  470                  475                  480  
 Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu  
                   485                  490                  495  
 Lys Pro Lys Val Ile His  
                   500

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2070 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 217..1812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATTATGAGA TGGAAGCATA GGTCAAAGCT GTTCCGGAGAA ATTGGAACTA CAGTTTTATC 60

TAGCCACATC TCTGAGAATT CTGAAGAAAG CAGCAGGTGA AAGTCATTGC CAAGTGATTT 120

TGTTCTGTAA GGAAGCCTCC CTCATTCACT TACACCAGTG AGACAGCAGG ACCAGTCATT 180

CAAAGGGCCG TGTACAGGAC GCGTGGCAAT CAGACA ATG ACT CAG CTA TAC ACT 234  
Met Thr Gln Leu Tyr Thr  
1 5

TAC ATC AGA TTA CTG GGA GCC TGT CTG TTC ATC ATT TCT CAT GTT CAA 282  
 Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe Ile Ile Ser His Val Gln  
           10                 15                 20

CCC CAG ATT GTC GAT AGT ATG CTG GAT CCC ACT CCT ATG AAA TGA GAC 330

Gly Gln Asn Leu Asp Ser Met Leu His Gly Thr Gly Met Lys Ser Asp			
25	30	35	
TTG GAC CAG AAG AAG CCA GAA AAT GGA GTG ACT TTA GCA CCA GAG GAT			378
Leu Asp Gln Lys Lys Pro Glu Asn Gly Val Thr Leu Ala Pro Glu Asp			
40	45	50	
ACC TTG CCT TTC TTA AAG TGC TAT TGC TCA GGA CAC TGC CCA GAT GAT			426
Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser Gly His Cys Pro Asp Asp			
55	60	65	70
GCT ATT AAT AAC ACA TGC ATA ACT AAT GGC CAT TGC TTT GCC ATT ATA			474
Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly His Cys Phe Ala Ile Ile			
75	80	85	
GAA GAA GAT GAT CAG GGA GAA ACC ACA TTA ACT TCT GGG TGT ATG AAG			522
Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu Thr Ser Gly Cys Met Lys			
90	95	100	
TAT GAA GGC TCT GAT TTT CAA TGC AAG GAT TCA CCG AAA GCC CAG CTA			570
Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp Ser Pro Lys Ala Gln Leu			
105	110	115	
CGC AGG ACA ATA GAA TGT TGT CGG ACC AAT TTG TGC AAC CAG TAT TTG			618
Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn Leu Cys Asn Gln Tyr Leu			
120	125	130	
CAG CCT ACA CTG CCC CCT GTT ATA GGT CCG TTC TTT GAT GGC AGC			666
Gln Pro Thr Leu Pro Pro Val Val Ile Gly Pro Phe Phe Asp Gly Ser			
135	140	145	150
ATC CGA TGG CTG GTT GTG CTC ATT TCC ATG GCT GTC TGT ATA GTT GCT			714
Ile Arg Trp Leu Val Val Leu Ile Ser Met Ala Val Cys Ile Val Ala			
155	160	165	
ATG ATC ATC TTC TCC AGC TGC TTT TGC TAT AAG CAT TAT TGT AAG AGT			762
Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr Lys His Tyr Cys Lys Ser			
170	175	180	
ATC TCA AGC AGG GGT CGT TAC AAC CGT GAT TTG GAA CAG GAT GAA GCA			810
Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp Leu Glu Gln Asp Glu Ala			
185	190	195	
TTT ATT CCA GTA GGA GAA TCA TTG AAA GAC CTG ATT GAC CAG TCC CAA			858
Phe Ile Pro Val Gly Glu Ser Leu Lys Asp Leu Ile Asp Gln Ser Gln			
200	205	210	
AGC TCT GGG AGT GGA TCT GGA TTG CCT TTA TTG GTT CAG CGA ACT ATT			906
Ser Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile			
215	220	225	230
GCC AAA CAG ATT CAG ATG GTT CGG CAG GTT GGT AAA GGC CGC TAT GGA			954
Ala Lys Gln Ile Gln Met Val Arg Gln Val Gly Lys Gly Arg Tyr Gly			
235	240	245	

GAA GTA TGG ATG GGT AAA TGG CGT GGT GAA AAA GTG GCT GTC AAA GTG Glu Val Trp Met Gly Lys Trp Arg Gly Glu Lys Val Ala Val Lys Val	250	255	260	1002
255	270	275		
TTT TTT ACC ACT GAA GAA GCT AGC TGG TTT AGA GAA ACA GAA ATC TAC Phe Phe Thr Thr Glu Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr	265			1050
270				
CAG ACG GTG TTA ATG CGT CAT GAA AAT ATA CTT GGT TTT ATA GCT GCA Gln Thr Val Leu Met Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala	280			1098
285				
GAC ATT AAA GGC ACT GGT TCC TGG ACT CAG CTG TAT TTG ATT ACT GAT Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp	295			1146
300				
305				
310				
TAC CAT GAA AAT GGA TCT CTC TAT GAC TTC CTG AAA TGT GCC ACA CTA Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe Leu Lys Cys Ala Thr Leu	315			1194
320				
325				
GAC ACC AGA GCC CTA CTC AAG TTA GCT TAT TCT GCT GCT TGT GGT CTG Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr Ser Ala Ala Cys Gly Leu	330			1242
335				
340				
TGC CAC CTC CAC ACA GAA ATT TAT GGT ACC CAA GGG AAG CCT GCA ATT Cys His Leu His Thr Glu Ile Tyr Gly Thr Gln Gly Lys Pro Ala Ile	345			1290
350				
355				
GCT CAT CGA GAC CTG AAG AGC AAA AAC ATC CTT ATT AAG AAA AAT GGA Ala His Arg Asp Leu Lys Ser Lys Asn Ile Leu Ile Lys Lys Asn Gly	360			1338
365				
370				
AGT TGC TGT ATT GCT GAC CTG GGC CTA GCT GTT AAA TTC AAC AGT GAT Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Lys Phe Asn Ser Asp	375			1386
380				
385				
390				
ACA AAT GAA GTT GAC ATA CCC TTG AAT ACC AGG GTG GGC ACC AAG CGG Thr Asn Glu Val Asp Ile Pro Leu Asn Thr Arg Val Gly Thr Lys Arg	395			1434
400				
405				
TAC ATG GCT CCA GAA GTG CTG GAT GAA AGC CTG AAT AAA AAC CAT TTC Tyr Met Ala Pro Glu Val Leu Asp Glu Ser Leu Asn Lys Asn His Phe	410			1482
415				
420				
CAG CCC TAC ATC ATG GCT GAC ATC TAT AGC TTT GGT TTG ATC ATT TGG Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser Phe Gly Leu Ile Ile Trp	425			1530
430				
435				
GAA ATG GCT CGT CGT TGT ATT ACA GGA GGA ATC GTG GAG GAA TAT CAA Glu Met Ala Arg Arg Cys Ile Thr Gly Gly Ile Val Glu Glu Tyr Gln	440			1578
445				
450				
TTA CCA TAT TAC AAC ATG GTG CCC AGT GAC CCA TCC TAT GAG GAC ATG Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp Pro Ser Tyr Glu Asp Met	460			1626
470				
480				

455	460	465	470	
CGT GAG GTT GTG TGT GTG AAA CGC TTG CGG CCA ATC GTG TCT AAC CGC				1674
Arg Glu Val Val Cys Val Lys Arg Leu Arg Pro Ile Val Ser Asn Arg				
475	480	485		
TGG AAC AGC GAT GAA TGT CTT CGA GCA GTT TTG AAG CTA ATG TCA GAA				1722
Trp Asn Ser Asp Glu Cys Leu Arg Ala Val Leu Lys Leu Met Ser Glu				
490	495	500		
TGT TGG GCC CAT AAT CCA GCC TCC AGA CTC ACA GCT TTG AGA ATC AAG				1770
Cys Trp Ala His Asn Pro Ala Ser Arg Leu Thr Ala Leu Arg Ile Lys				
505	510	515		
AAG ACA CTT GCA AAA ATG GTT GAA TCC CAG GAT GTA AAG ATT				1812
Lys Thr Leu Ala Lys Met Val Glu Ser Gln Asp Val Lys Ile				
520	525	530		
TGACAATTAA ACAATTGTGA GGGAGAATT AGACTGCAAG AACTTCTTCA CCCAAGGAAT				1872
GGGTGGGATT AGCATGGAAT AGGATGTTGA CTTGGTTCC AGACTCCTTC CTCTACATCT				1932
TCACAGGCTG CTAACAGTAA ACCTTACCGT ACTCTACAGA ATACAAGATT GGAACTTGGA				1992
ACTTCAAACA TGTCATTCTT TATATATGAC AGCTTGTTT TAATGTGGGG TTTTTTGTT				2052
TGCTTTTTT GTTTGTT				2070

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Thr Gln Leu Tyr Thr Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe			
1	5	10	15
Ile Ile Ser His Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly			
20	25	30	
Thr Gly Met Lys Ser Asp Leu Asp Gln Lys Lys Pro Glu Asn Gly Val			
35	40	45	
Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser			
50	55	60	
Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly			
65	70	75	80
His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu			
85	90	95	
Thr Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp			
100	105	110	
Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn			

115                    120                    125  
Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly  
130                    135                    140  
Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Val Leu Ile Ser Met  
145                    150                    155                    160  
Ala Val Cys Ile Val Ala Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr  
165                    170                    175  
Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp  
180                    185                    190  
Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp  
195                    200                    205  
Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu  
210                    215                    220  
Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val  
225                    230                    235                    240  
Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu  
245                    250                    255  
Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe  
260                    265                    270  
Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile  
275                    280                    285  
Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln  
290                    295                    300  
Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe  
305                    310                    315                    320  
Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr  
325                    330                    335  
Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr  
340                    345                    350  
Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile  
355                    360                    365  
Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala  
370                    375                    380  
Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Ile Pro Leu Asn Thr  
385                    390                    395                    400  
Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser  
405                    410                    415  
Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser  
420                    425                    430  
Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly  
435                    440                    445  
Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp  
450                    455                    460  
Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg  
465                    470                    475                    480  
Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val  
485                    490                    495  
Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu  
500                    505                    510  
Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln  
515                    520                    525  
Asp Val Lys Ile  
530

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2160 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 10..1524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CGCGGGTTAC ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT	48
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu	
1 5 10	
GTT GTC CTC CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG ATC	96
Val Val Leu Leu Leu Ala Gly Ser Gly Ser Gly Pro Arg Gly Ile	
15 20 25	
CAG GCT CTG CTG TGT GCG TGC ACC AGC TGC CTA CAG ACC AAC TAC ACC	144
Gln Ala Leu Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr	
30 35 40 45	
TGT GAG ACA GAT GGG GCT TGC ATG GTC TCC ATC TTT AAC CTG GAT GGC	192
Cys Glu Thr Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly	
50 55 60	
GTG GAG CAC CAT GTA CGT ACC TGC ATC CCC AAG GTG GAG CTG GTT CCT	240
Val Glu His His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro	
65 70 75	
GCT GGA AAG CCC TTC TAC TGC CTG AGT TCA GAG GAT CTG CGC AAC ACA	288
Ala Gly Lys Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr	
80 85 90	
CAC TGC TGC TAT ATT GAC TTC TGC AAC AAG ATT GAC CTC AGG GTC CCC	336
His Cys Cys Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro	
95 100 105	
AGC GGA CAC CTC AAG GAG CCT GCG CAC CCC TCC ATG TGG GGC CCT GTG	384
Ser Gly His Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val	

110	115	120	125	
GAG CTG GTC GGC ATC ATC GCC GGC CCC GTC TTC CTC CTC TTC CTT ATC Glu Leu Val Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile 130	135		140	432
ATT ATC ATC GTC TTC CTG GTC ATC AAC TAT CAC CAG CGT GTC TAC CAT Ile Ile Ile Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His 145	150	155		480
AAC CGC CAG AGG TTG GAC ATG GAG GAC CCC TCT TGC GAG ATG TGT CTC Asn Arg Gln Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu 160	165	170		528
TCC AAA GAC AAG ACG CTC CAG GAT CTC GTC TAC GAC CTC TCC ACG TCA Ser Lys Asp Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser 175	180	185		576
GGG TCT GGC TCA GGG TTA CCC CTT TTT GTC CAG CGC ACA GTG GCC CGA Gly Ser Gly Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg 190	195	200	205	624
ACC ATT GTT TTA CAA GAG ATT ATC GGC AAG GGC CGG TTC GGG GAA GTA Thr Ile Val Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val 210	215	220		672
TGG CGT GGT CGC TGG AGG GGT GGT GAC GTG GCT GTG AAA ATC TTC TCT Trp Arg Gly Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser 225	230	235		720
TCT CGT GAA GAA CGG TCT TGG TTC CGT GAA GCA GAG ATC TAC CAG ACC Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr 240	245	250		768
GTC ATG CTG CGC CAT GAA AAC ATC CTT GGC TTT ATT GCT GCT GAC AAT Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn 255	260	265		816
AAA GAT AAT GGC ACC TGG ACC CAG CTG TGG CTT GTC TCT GAC TAT CAC Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His 270	275	280	285	864
GAG CAT GGC TCA CTG TTT GAT TAT CTG AAC CGC TAC ACA GTG ACC ATT Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile 290	295	300		912
GAG GGA ATG ATT AAG CTA GCC TTG TCT GCA GCC AGT GGT TTG GCA CAC Glu Gly Met Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His 305	310	315		960
CTG CAT ATG GAG ATT GTG GGC ACT CAA GGG AAG CCG GGA ATT GCT CAT Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His 320	325	330		1008

CGA GAC TTG AAG TCA AAG AAC ATC CTG GTG AAA AAA AAT GGC ATG TGT Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys 335                   340                   345	1056
GCC ATT GCA GAC CTG GGC CTG GCT GTC CGT CAT GAT GCG GTC ACT GAC Ala Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp 350                   355                   360                   365	1104
ACC ATA GAC ATT GCT CCA AAT CAG AGG GTG GGG ACC AAA CGA TAC ATG Thr Ile Asp Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met 370                   375                   380	1152
GCT CCT GAA GTC CTT GAC GAG ACA ATC AAC ATG AAG CAC TTT GAC TCC Ala Pro Glu Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser 385                   390                   395	1200
TTC AAA TGT GCC GAC ATC TAT GCC CTC GGG CTT GTC TAC TGG GAG ATT Phe Lys Cys Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile 400                   405                   410	1248
GCA CGA AGA TGC AAT TCT GGA GGA GTC CAT GAA GAC TAT CAA CTG CCG Ala Arg Arg Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro 415                   420                   425	1296
TAT TAC GAC TTA GTG CCC TCC GAC CCT TCC ATT GAG GAG ATG CGA AAG Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys 430                   435                   440                   445	1344
GTT GTA TGT GAC CAG AAG CTA CGG CCC AAT GTC CCC AAC TGG TGG CAG Val Val Cys Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln 450                   455                   460	1392
AGT TAT GAG GCC TTG CGA GTG ATG GGA AAG ATG ATG CGG GAG TGC TGG Ser Tyr Glu Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp 465                   470                   475	1440
TAC GCC AAT GGT GCT GCC CGT CTG ACA GCT CTG CGC ATC AAG AAG ACT Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr 480                   485                   490	1488
CTG TCC CAG CTA AGC GTG CAG GAA GAT GTG AAG ATT TAAGCTGTT Leu Ser Gln Leu Ser Val Gln Glu Asp Val Lys Ile 495                   500                   505	1534
CTCTGCCTAC ACAAGAACCGGGCAGTGA GGATGACTGC AGCCACCGTG CAAGCGTCGT GGAGGCCTAT CCTCTTGTCTT CTGCCGGCC CTCTGGCAGA GCCCTGGCCT GCAAGAGGGA	1594
CAGAGCCTGG GAGACGCGCG CACTCCCAGTGGTT GGGTTTGAGA CAGACACTTT TTATATTAC	1654
CTCCTGATGG CATGGAGACC TGAGCAAATC ATGTAGTCAC TCAATGCCAC AACTCAAAC	1714
GCTTCAGTGG GAAGTACAGA GACCCAGTGC ATTGCGTGTG CAGGAGCGTG AGGTGCTGGG	1774
	1834

CTGCCAGGA GCGGCCCCA TACCTGTGG TCCACTGGC TGCAGGTTT CCTCCAGGGA	1894
CCAGTCAACT GGCATCAAGA TATTGAGAGG AACCGGAAGT TTCTCCCTCC TTCCCGTAGC	1954
AGTCCTGAGC CACACCCTCC TTCTCATGGA CATCCGGAGG ACTGCCCTA GAGACACAAC	2014
CTGCTGCCTG TCTGTCCAGC CAAGTGCGCA TGTGCCGAGG TGTGTCCCAC ATTGTGCCTG	2074
GTCTGTGCCA CGCCCGTGTG TGTGTGTGTG TGTGTGAGTG AGTGTGTGTG TGTACACTTA	2134
ACCTGCTTGA GCTTCTGTGC ATGTGT	2160

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu
      1           5           10          15
Leu Leu Ala Gly Ser Gly Ser Gly Pro Arg Gly Ile Gln Ala Leu
      20          25          30
Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr Cys Glu Thr
      35          40          45
Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly Val Glu His
      50          55          60
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys
      65          70          75          80
Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys
      85          90          95
Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro Ser Gly His
      100         105         110
Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val Glu Leu Val
      115         120         125
Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile
      130         135         140
Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln
      145         150         155         160
Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp
      165         170         175
Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly
      180         185         190
Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val
      195         200         205
Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly
      210         215         220
Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu
      225         230         235         240
Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu

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245	250	255
Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn		
260	265	270
Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly		
275	280	285
Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met		
290	295	300
Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met		
305	310	315
Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu		
325	330	335
Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala		
340	345	350
Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp		
355	360	365
Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu		
370	375	380
Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys		
385	390	395
Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg		
405	410	415
Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp		
420	425	430
Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys		
435	440	445
Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln Ser Tyr Glu		
450	455	460
Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn		
465	470	475
Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln		
485	490	495
Leu Ser Val Gln Glu Asp Val Lys Ile		
500	505	

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1952 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 187..1692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AAGCGGCGGC AGAACGGTGC	GGCGTGGTGC TCGTAGTGAG	GGCGCGGAGG ACCCGGGACC	60
TGGGAAGCGG CGGC GGTTA	ACTTCGGCTG AATCACAAACC	ATTGGCGCT GAGCTATGAC	120
AAGAGAGCAA ACAAAAAGTT	AAAGGAGCAA CCCGCCATA	AGTGAAGAGA GAAGTTTATT	180
GATAAC ATG CTC TTA CGA AGC	TCT GGA AAA TTA AAT GTG	GGC ACC AAG	228
Met Leu Leu Arg Ser Ser	Gly Lys Leu Asn Val	Gly Thr Lys	
1 . . . . .	5 . . . . .	10 . . . . .	
AAG GAG GAT GGA GAG	AGT ACA GCC CCC ACC CCT	CGG CCC AAG ATC CTA	276
Lys Glu Asp Gly Glu	Ser Thr Ala Pro Thr	Pro Arg Pro Lys Ile Leu	
15 . . . . .	20 . . . . .	25 . . . . .	30 . . . . .
CGT TGT AAA TGC CAC	CAC CAC TGT CCG GAA GAC	TCA GTC AAC AAT ATC	324
Arg Cys Lys Cys His	His Cys Pro Glu Asp	Ser Val Asn Asn Ile	
35 . . . . .	40 . . . . .	45 . . . . .	
TGC AGC ACA GAT GGG	TAC TGC TTC ACG ATG ATA	GAA GAA GAT GAC TCT	372
Cys Ser Thr Asp Gly	Tyr Cys Phe Thr Met	Ile Glu Glu Asp Asp Ser	
50 . . . . .	55 . . . . .	60 . . . . .	
GGA ATG CCT GTT GTC	ACC TCT GGA TGT CTA	GAA CTA GAA GGG TCA GAT	420
Gly Met Pro Val Val	Thr Ser Gly Cys Leu	Gly Leu Glu Gly Ser Asp	
65 . . . . .	70 . . . . .	75 . . . . .	
TTT CAA TGT CGT GAC	ACT CCC ATT CCT CAT CAA	AGA AGA TCA ATT GAA	468
Phe Gln Cys Arg Asp	Thr Pro Ile Pro His Gln	Arg Arg Ser Ile Glu	
80 . . . . .	85 . . . . .	90 . . . . .	
TGC TGC ACA GAA AGG	AAT GAG TGT AAT AAA	GAC CTC CAC CCC ACT CTG	516
Cys Cys Thr Glu Arg	Asn Glu Cys Asn Lys	Asp Leu His Pro Thr Leu	
95 . . . . .	100 . . . . .	105 . . . . .	110 . . . . .
CCT CCT CTC AAG GAC	AGA GAT TTT GTT GAT	GGG CCC ATA CAC CAC AAG	564
Pro Pro Leu Lys Asp	Arg Asp Phe Val Asp	Gly Pro Ile His His Lys	
115 . . . . .	120 . . . . .	125 . . . . .	
GCC TTG CTT ATC TCT	GTG ACT GTC TGT AGT	TTA CTC TTG GTC CTC ATT	612
Ala Leu Leu Ile Ser	Val Thr Val Cys Ser	Leu Leu Leu Val Leu Ile	
130 . . . . .	135 . . . . .	140 . . . . .	
ATT TTA TTC TGT TAC	TTC AGG TAT AAA AGA	CAA GAA GCC CGA CCT CGG	660
Ile Leu Phe Cys Tyr	Phe Arg Tyr Lys Arg	Gln Glu Ala Arg Pro Arg	
145 . . . . .	150 . . . . .	155 . . . . .	
TAC AGC ATT GGG CTG	GAG CAG GAC GAG	ACA TAC ATT CCT CCT GGA GAG	708
Tyr Ser Ile Gly Leu	Glu Gln Asp Glu	Thr Tyr Ile Pro Pro Gly Glu	
160 . . . . .	165 . . . . .	170 . . . . .	

TCC CTG AGA GAC TTG ATC GAG CAG TCT CAG AGC TCG GGA AGT GGA TCA Ser Leu Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser 175                   180                   185                   190	756
GGC CTC CCT CTG CTG GTC CAA AGG ACA ATA GCT AAG CAA ATT CAG ATG Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met 195                   200                   205	804
GTC AAG CAG ATT GGA AAA GGC CGC TAT GGC GAG GTG TGG ATG GGA AAG Val Lys Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys 210                   215                   220	852
TGG CGT GGA GAA AAG GTG GCT GTG AAA GTG TTC TTC ACC ACG GAG GAA Trp Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu 225                   230                   235	900
GCC AGC TGG TTC CGA GAG ACT GAG ATA TAT CAG ACG GTC CTG ATG CGG Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg 240                   245                   250	948
CAT GAG AAT ATT CTG GGG TTC ATT GCT GCA GAT ATC AAA GGG ACT GGG His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly 255                   260                   265                   270	996
TCC TGG ACT CAG TTG TAC CTC ATC ACA GAC TAT CAT GAA AAC GGC TCC Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser 275                   280                   285	1044
CTT TAT GAC TAT CTG AAA TCC ACC ACC TTA GAC GCA AAG TCC ATG CTG Leu Tyr Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu 290                   295                   300	1092
AAG CTA GCC TAC TCC TCT GTC AGC GGC CTA TGC CAT TTA CAC ACG GAA Lys Leu Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu 305                   310                   315	1140
ATC TTT AGC ACT CAA GGC AAG CCA GCA ATC GCC CAT CGA GAC TTG AAA Ile Phe Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys 320                   325                   330	1188
AGT AAA AAC ATC CTG GTG AAG AAA AAT GGA ACT TGC TGC ATA GCA GAC Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp 335                   340                   345                   350	1236
CTG GGC TTG GCT GTC AAG TTC ATT AGT GAC ACA AAT GAG GTT GAC ATC Leu Gly Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile 355                   360                   365	1284
CCA CCC AAC ACC CGG GTT GGC ACC AAG CGC TAT ATG CCT CCA GAA GTG Pro Pro Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val 370                   375                   380	1332
CTG GAC GAG AGC TTG AAT AGA AAC CAT TTC CAG TCC TAC ATT ATG GCT Leu Asp Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala	1380

385

390

395

GAC ATG TAC AGC TTT GGA CTC ATC CTC TGG GAG ATT GCA AGG AGA TGT Asp Met Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys 400 405 410	1428
GTT TCT GGA GGT ATA GTG GAA GAA TAC CAG CTT CCC TAT CAC GAC CTG Val Ser Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu 415 420 425 430	1476
GTG CCC AGT GAC CCT TCT TAT GAG GAC ATG AGA GAA ATT GTG TGC ATG Val Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met 435 440 445	1524
AAG AAG TTA CGG CCT TCA TTC CCC AAT CGA TGG AGC AGT GAT GAG TGT Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys 450 455 460	1572
CTC AGG CAG ATG GGG AAG CTT ATG ACA GAG TGC TGG GCG CAG AAT CCT Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro 465 470 475	1620
GCC TCC AGG CTG ACG GCC CTG AGA GTT AAG AAA ACC CTT GCC AAA ATG Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met 480 485 490	1668
TCA GAG TCC CAG GAC ATT AAA CTC TGACGTCAGA TACTTGTGGA CAGAGCAAGA Ser Glu Ser Gln Asp Ile Lys Leu 495 500	1722
ATTCACAGA AGCATCGTTA GCCCAAGCCT TGAACGTTAG CCTACTGCC AGTGAGTTCA	1782
GACTTCTG GAAGAGAGCA CGGTGGCAG ACACAGAGGA ACCCAGAAAC ACGGATTCA	1842
CATGGCTTTC TGAGGAGGAG AAACGTGTTG GGTAACTTGT TCAAGATATG ATGCATGTTG	1902
CTTCTAAGA AAGCCCTGTA TTTTGAATTA CCATTTTTT ATAAAAAAA	1952

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys Lys Glu 1 5 10 15
Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu Arg Cys 20 25 30
Lys Cys His His Cys Pro Glu Asp Ser Val Asn Asn Ile Cys Ser

35                    40                    45  
Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Met  
50                    55                    60  
Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp Phe Gln  
65                    70                    75                    80  
Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys  
85                    90                    95  
Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro  
100                  105                  110  
Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys Ala Leu  
115                  120                  125  
Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu  
130                  135                  140  
Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg Tyr Ser  
145                  150                  155                  160  
Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu  
165                  170                  175

Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu  
                  180                 185                 190  
 Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys  
                  195                 200                 205  
 Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg  
                  210                 215                 220  
 Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser  
                  225                 230                 235                 240  
 Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu  
                  245                 250                 255  
 Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp  
                  260                 265                 270  
 Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr  
                  275                 280                 285  
 Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu  
                  290                 295                 300  
 Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe  
                  305                 310                 315                 320  
 Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys  
                  325                 330                 335  
 Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly  
                  340                 345                 350  
 Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro  
                  355                 360                 365  
 Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp  
                  370                 375                 380  
 Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala Asp Met  
                  385                 390                 395                 400  
 Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys Val Ser  
                  405                 410                 415  
 Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro  
                  420                 425                 430  
 Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met Lys Lys  
                  435                 440                 445  
 Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys Leu Arg  
                  450                 455                 460  
 Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro Ala Ser  
                  465                 470                 475                 480  
 Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met Ser Glu  
                  485                 490                 495  
 Ser Gln Asp Ile Lys Leu  
                  500

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GCGGATCCTG TTGTGAAGGN AATATGTG

28

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GCGATCCGTC GCAGTCAAAA TTTT

24

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCGGATCCGC GATATATTAA AAGCAA

26

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CGGAATTCTG GTGCCATATA

20

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATTCAAGGGC ACATCAACTT CATTGTGTC ACTGTTG

37

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GCGGATCCAC CATGGCGGAG TCGGCC

26

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AACACCGGGC CGGCGATGAT

20

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gly Xaa Gly Xaa Xaa Gly  
1 5

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Asp Phe Lys Ser Arg Asn  
1 5

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Asp Leu Lys Ser Lys Asn  
1 5

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Gly Thr Lys Arg Tyr Met  
1                       5

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 182 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Leu Asp Thr Leu Val Gly Lys Gly Arg Phe Ala Glu Val Tyr Lys Ala  
5                       10                       15  
Lys Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu Thr Val Ala Val Lys  
20                      25                       30  
Ile Phe Pro Tyr Asp His Tyr Ala Ser Trp Lys Asp Arg Lys Asp Ile  
35                      40                       45  
Phe Ser Asp Ile Asn Leu Lys His Glu Asn Ile Leu Gln Phe Leu Thr  
50                      55                       60  
Ala Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln Tyr Trp Leu Ile Thr  
65                      70                       75                       80  
Ala Phe His Ala Lys Gly Asn Leu Gln Glu Tyr Leu Thr Arg His Val  
85                      90                       95  
Ile Ser Trp Glu Asp Leu Arg Asn Val Gly Ser Ser Leu Ala Arg Gly  
100                     105                      110  
Leu Ser His Leu His Ser Asp His Thr Pro Cys Gly Arg Pro Lys Met  
115                     120                      125  
Pro Ile Val His Arg Asp Leu Lys Ser Ser Asn Ile Leu Val Lys Asn  
130                     135                      140  
Asp Leu Thr Cys Cys Leu Cys Asp Phe Gly Leu Ser Leu Arg Leu Gly  
145                     150                      155                       160  
Pro Tyr Ser Ser Val Asp Asp Leu Ala Asn Ser Gly Gln Val Gly Thr  
165                     170                      175  
Ala Arg Tyr Met Ala Pro  
180

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 176 amino acids
  - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Leu Leu Glu Ile Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala  
5 10 15  
Gln Leu Met Asn Asp Phe Val Ala Val Lys Ile Phe Pro Leu Gln Asp  
20 25 30  
Lys Gln Ser Trp Gln Ser Glu Arg Glu Ile Phe Ser Thr Pro Gly Met  
35 40 45  
Lys His Glu Asn Leu Leu Gln Phe Ile Ala Ala Glu Lys Arg Gly Ser  
50 55 60  
Asn Leu Glu Val Glu Leu Trp Leu Ile Thr Ala Phe His Asp Lys Gly  
65 70 75 80  
Ser Leu Thr Asp Tyr Leu Lys Gly Asn Ile Ile Thr Trp Asn Glu Leu  
85 90 95  
Cys His Val Ala Glu Thr Met Ser Arg Gly Leu Ser Tyr Leu His Glu  
100 105 110  
Asp Val Pro Trp Cys Arg Gly Glu Gly His Lys Pro Ser Ile Ala His  
115 120 125  
Arg Asp Phe Lys Ser Lys Asn Val Leu Leu Lys Ser Asp Leu Thr Ala  
130 135 140  
Val Leu Ala Asp Phe Gly Leu Ala Val Arg Phe Glu Pro Gly Lys Pro  
145 150 155 160  
Pro Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro  
165 170 175

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala  
5 10 15  
Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln Asp  
20 25 30  
Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly Met  
35 40 45  
Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly Thr  
50 55 60

Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys Gly  
 65                   70                   75                   80  
 Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu Leu  
       85              90              95  
 Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His Glu  
       100            105            110  
 Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His Arg  
       115            120            125  
 Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala Cys  
       130            135            140  
 Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser Ala  
 145                150              155                160  
 Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro  
       165            170            175

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 178 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *C. elegans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Leu Thr Gly Arg Val Gly Ser Gly Arg Phe Gly Asn Val Ser Arg Gly  
       5               10               15  
 Asp Tyr Arg Gly Glu Ala Val Ala Val Lys Val Phe Asn Ala Leu Asp  
       20              25              30  
 Glu Pro Ala Phe His Lys Glu Thr Glu Ile Phe Glu Thr Arg Met Leu  
       35              40              45  
 Arg His Pro Asn Val Leu Arg Tyr Ile Gly Ser Asp Arg Val Asp Thr  
       50              55              60  
 Gly Phe Val Thr Glu Leu Trp Leu Val Thr Glu Tyr His Pro Ser Gly  
 65                70                75                80  
 Ser Leu His Asp Phe Leu Leu Glu Asn Thr Val Asn Ile Glu Thr Tyr  
       85              90              95  
 Tyr Asn Leu Met Arg Ser Thr Ala Ser Gly Leu Ala Phe Leu His Asn  
       100             105             110  
 Gln Ile Gly Gly Ser Lys Glu Ser Asn Lys Pro Ala Met Ala His Arg  
       115             120             125  
 Asp Ile Lys Ser Lys Asn Ile Met Val Lys Asn Asp Leu Thr Cys Ala  
       130             135             140  
 Ile Gly Asp Leu Gly Leu Ser Leu Ser Lys Pro Glu Asp Ala Ala Ser  
 145                150              155                160  
 Asp Ile Ile Ala Asn Glu Asn Tyr Lys Cys Gly Thr Val Arg Tyr Leu  
       165            170            175

Ala Pro

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: MOUSE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys  
               5                    10                    15  
 Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe  
               20                    25                    30  
 Phe Asn Ala Asn Trp Glu lys Asp Arg Thr Asn Gln Thr Gly Val Glu  
               35                    40                    45  
 Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp  
               50                    55                    60  
 Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu  
               65                    70                    75                    80  
 Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu Lys Lys Asp  
               85                    90                    95  
 Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu  
               100                    105                    110  
 Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn  
               115                    120                    125  
 Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu  
               130                    135                    140  
 Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val  
               145                    150                    155                    160  
 Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln  
               165                    170                    175  
 Asp Pro Gly Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu  
               180                    185                    190  
 Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys  
               195                    200                    205  
 Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln  
               210                    215                    220  
 Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly  
               225                    230                    235                    240  
 Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly  
               245                    250                    255  
 Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys  
               260                    265                    270  
 Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu  
               275                    280                    285  
 Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His  
               290                    295                    300  
 Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His  
               305                    310                    315                    320

Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala  
325 330 335  
Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser  
340 345 350  
Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro  
355 360 365  
Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg  
370 375 380  
Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg  
385 390 395 400  
Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu  
405 410 415  
Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val  
420 425 430  
Val His Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His  
435 440 445  
Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His  
450 455 460  
Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr  
465 470 475 480  
Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr  
485 490 495  
Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser  
500 505 510  
Leu

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 536 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: MOUSE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Met Thr Ala Pro Trp Ala Ala Leu Ala Leu Leu Trp Gly Ser Leu Cys  
5 10 15  
  
Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr  
20 25 30  
Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg  
35 40 45  
Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Arg  
50 55 60  
Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp  
65 70 75 80  
Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn  
85 90 95

Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg  
100 105 110  
Phe Thr His Leu Pro Glu Pro Gly Gly Pro Glu Val Thr Tyr Glu Pro  
115 120 125  
Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu  
130 135 140  
Pro Ile Gly Gly Leu Ser Ile Val Leu Leu Ala Phe Trp Met Tyr  
145 150 155 160  
Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Val Arg  
165 170 175  
Gln Cys Gln Arg Trp Ala Gly Arg Asp Gly Cys Ala Asp Ser Phe  
180 185 190  
Lys Pro Leu Pro Phe Gln Asp Pro Gly Pro Pro Pro Ser Pro Leu  
195 200 205  
Val Gly Leu Lys Pro Leu Gln Leu Leu Glu Ile Lys Ala Arg Gly Arg  
210 215 220  
Phe Gly Cys Val Trp Lys Ala Gln Leu Met Asn Asp Phe Val Ala Val  
225 230 235 240  
Lys Ile Phe Pro Leu Gln Asp Lys Gln Ser Trp Gln Ser Glu Arg Glu  
245 250 255  
Ile Phe Ser Thr Pro Gly Met Lys His Glu Asn Leu Leu Gln Phe Ile  
260 265 270  
Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu Val Glu Leu Trp Leu Ile  
275 280 285  
Thr Ala Phe His Asp Lys Gly Ser Leu Thr Asp Tyr Leu Lys Gly Asn  
290 295 300  
Ile Ile Thr Trp Asn Glu Leu Cys His Val Ala Glu Thr Met Ser Arg  
305 310 315 320  
Gly Leu Ser Tyr Leu His Glu Asp Val Pro Trp Cys Arg Gly Glu Gly  
325 330 335  
His Lys Pro Ser Ile Ala His Arg Asp Phe Lys Ser Lys Asn Val Leu  
340 345 350  
Leu Lys Ser Asp Leu Thr Ala Val Leu Ala Asp Phe Gly Leu Ala Val  
355 360 365  
Arg Phe Glu Pro Gly Lys Pro Pro Gly Asp Thr His Gly Gln Val Gly  
370 375 380  
Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe  
385 390 395 400  
Gln Arg Asp Ala Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val  
405 410 415  
Leu Trp Glu Leu Val Ser Arg Cys Lys Ala Ala Asp Gly Pro Val Asp  
420 425 430  
Glu Tyr Met Leu Pro Phe Glu Glu Glu Ile Gly Gln His Pro Ser Leu  
435 440 445  
Glu Glu Leu Gln Glu Val Val His Lys Lys Met Arg Pro Thr Ile  
450 455 460  
Lys Asp His Trp Leu Lys His Pro Gly Leu Ala Gln Leu Cys Val Thr  
465 470 475 480  
Ile Glu Glu Cys Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly  
485 490 495  
Cys Val Glu Glu Arg Val Ser Leu Ile Arg Arg Ser Val Asn Gly Thr  
500 505 510  
Thr Ser Asp Cys Leu Val Ser Leu Val Thr Ser Val Thr Asn Val Asp  
515 520 525

Leu Leu Pro Lys Glu Ser Ser Ile  
530                           535

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 567 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Met Gly Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val Leu  
5                                 10                                 15  
Trp Thr Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln Lys Ser Val  
20                                 25                                 30  
Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro  
35                                 40                                 45  
Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln  
50                                 55                                 60  
Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro  
65                                 70                                 75                                 80  
Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr  
85                                 90                                 95  
Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile  
100                                 105                                 110  
Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys  
115                                 120                                 125  
Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn  
130                                 135                                 140  
Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu  
145                                 150                                 155                                 160  
Leu Leu Val Ile Phe Gln Val Thr Gly Ile Ser Leu Leu Pro Pro Leu  
165                                 170                                 175  
Gly Val Ala Ile Ser Val Ile Ile Phe Tyr Cys Tyr Arg Val Asn  
180                                 185                                 190  
Arg Gln Gln Lys Leu Ser Ser Thr Trp Glu Thr Gly Lys Thr Arg Lys  
195                                 200                                 205  
Leu Met Glu Phe Ser Glu His Cys Ala Ile Ile Leu Glu Asp Asp Arg  
210                                 215                                 220  
Ser Asp Ile Ser Ser Thr Cys Ala Asn Asn Ile Asn His Asn Thr Glu  
225                                 230                                 235                                 240  
Leu Leu Pro Ile Glu Leu Asp Thr Leu Val Gly Lys Gly Arg Phe Ala  
245                                 250                                 255  
Glu Val Tyr Lys Ala Lys Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu  
260                                 265                                 270  
Thr Val Ala Val Lys Ile Phe Pro Tyr Glu Glu Tyr Ala Ser Trp Lys  
275                                 280                                 285  
Thr Glu Lys Asp Ile Phe Ser Asp Ile Asn Leu Lys His Glu Asn Ile

290	295	300
Leu Gln Phe Leu Thr Ala Glu Glu Arg Lys	Thr Glu Leu Gly Lys Gln	
305	310	315
Tyr Trp Leu Ile Thr Ala Phe His Ala Lys	Gly Asn Leu Gln Glu Tyr	
325	330	335
Leu Thr Arg His Val Ile Ser Trp Glu Asp	Leu Arg Lys Leu Gly Ser	
340	345	350
Ser Leu Ala Arg Gly Ile Ala His	Leu His Ser Asp His Thr Pro Cys	
355	360	365
Gly Arg Pro Lys Met Pro Ile Val His Arg	Asp Leu Lys Ser Ser Asn	
370	375	380
Ile Leu Val Lys Asn Asp Leu Thr Cys	Cys Leu Cys Asp Phe Gly Leu	
385	390	395
Ser Leu Arg Leu Asp Pro Thr Leu Ser Val	Asp Asp Leu Ala Asn Ser	
405	410	415
Gly Gln Val Gly Thr Ala Arg Tyr Met Ala	Pro Glu Val Leu Glu Ser	
420	425	430
Arg Met Asn Leu Glu Asn Ala Glu Ser	Phe Lys Gln Thr Asp Val Tyr	
435	440	445
Ser Met Ala Leu Val Leu Trp Glu Met Thr	Ser Arg Cys Asn Ala Val	
450	455	460
Gly Glu Val Lys Asp Tyr Glu Pro Pro Phe	Gly Ser Lys Val Arg Glu	
465	470	475
His Pro Cys Val Glu Ser Met Lys Asp Asn	Val Leu Arg Asp Arg Gly	
485	490	495
Arg Pro Glu Ile Pro Ser Phe Trp Leu Asn	His Gln Gly Ile Gln Met	
500	505	510
Val Cys Glu Thr Leu Thr Glu Cys Trp Asp	His Asp Pro Glu Ala Arg	
515	520	525
Leu Thr Ala Gln Cys Val Ala Glu Arg Phe	Ser Glu Leu Glu His Leu	
530	535	540
Asp Arg Leu Ser Gly Arg Ser Cys Ser Glu	Glu Lys Ile Pro Glu Asp	
545	550	555
Gly Ser Leu Asn Thr Thr Lys		560
	565	

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 97 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: C. elegans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Cys His Cys Ser Arg Glu Val Gly Cys Asn Ala Arg Thr	Thr Gly Trp	
5	10	15
Val Pro Gly Ile Glu Phe Leu Asn Glu	Thr Asp Arg Ser	Phe Tyr Glu

20                    25                    30  
Asn Thr Cys Tyr Thr Asp Gly Ser Cys Tyr Gln Ser Ala Arg Pro Ser  
      35                    40                    45  
Pro Glu Ile Ser His Phe Gly Cys Met Asp Glu Lys Ser Val Thr Asp  
      50                    55                    60  
Glu Thr Glu Phe His Asp Thr Ala Ala Lys Val Cys Thr Asn Asn Thr  
      65                    70                    75                    80  
Lys Asp Pro His Ala Thr Val Trp Ile Cys Cys Asp Lys Gly Asn Phe  
      85                    90                    95  
Cys

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Asp Leu Lys Pro Glu Asn  
      5

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Asp Leu Ala Ala Arg Asn  
      5

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Asp Ile Lys Ser Lys Asn

5

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Asp Phe Lys Ser Lys Asn

5

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Asp Leu Lys Ser Ser Asn

5

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (D) OTHER INFORMATION: First Xaa is Thr or Ser; fourth Xaa is Tyr or Phe; Each other Xaa may be any amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Gly Xaa Xaa Xaa Xaa Xaa

5

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids

- (B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: First Xaa is any amino acid;  
second Xaa is Ile or Val;  
third Xaa is Lys or Arg;  
fourth Xaa is Thr or Met.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Xaa Pro Xaa Xaa Trp Xaa  
5

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Gly Thr Arg Arg Tyr Met  
5

E3  
*Cont*  
(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Gly Thr Ala Arg Tyr Met  
5